

GenCore version 4.5
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OM nucleic - nucleic search, using sw model
Run on: November 25, 2000, 03:51:15 ; Search time 853.82 Seconds
(scoring table: IDENTITY_NUC (without alignments)
3410.674 Million cell updates/sec)

Title: US-09-373-230-1
Perfect score: 471
Sequence: 1 AACTTGGCCGACTTCAGT.....TCACTAACTTACATCAAAGT 471

Scoring table: Gapop 10.0 , Gapext 1.0

Searched: 7189864 seqs, 3091403243 residues

Total number of hits satisfying chosen parameters: 14379728

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*

1: gb_est1:*
2: gb_est2:*
3: gb_est3:*
4: gb_est4:*
5: gb_est5:*
6: gb_est6:*
7: gb_est7:*
8: gb_est8:*
9: gb_est9:*
10: gb_est10:*
11: gb_est11:*
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13: gb_est13:*
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113: gb_gss14:*
114: gb_gss15:*
115: gb_gss16:*
116: gb_gss17:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES							
Result No.	Score	Query Match	Length	DB	ID	Description	
1	465.8	98.9	603	7	AA930362	AA930362 vs59f07.r	
2	400.6	85.1	646	7	AA892285	AA892285 EST196088	
3	365.6	77.6	512	20	AW125102	AW125102 UI-M-BH2.	
4	337.6	71.7	474	8	AII121020	AII121020 ud69c02.x	
5	308.6	65.5	434	2	AA237736	AA237736 mx29g01.r	
6	274	58.2	469	10	AI463005	AI463005 vb89g05.x	
7	260.8	55.4	423	23	AW558748	AW558748 L0299E02-	
8	239.8	50.9	443	19	AV597984	AV597984 AV597984	
9	208	44.2	357	19	AW049334	AW049334 UI-M-BH1-	
10	207.4	44.0	369	9	AI176343	AI176343 EST21926	
11	197.4	41.9	342	13	AI1835755	AI1835755 UI-M-A10-	
12	191.6	40.7	335	15	AV066410	AV066410 AV066410	
13	173.4	36.8	289	2	AA245600	AA245600 mx30a01.r	
14	166.8	35.4	505	8	AI046315	AI046315 ud69c02.y	
15	155.6	33.0	574	19	AV597985	AV597985 AV597985	
16	153.8	32.7	294	15	AV072353	AV072353	
17	153.8	32.7	354	12	AI642457	AI642457 vv80b10.x	
18	153.4	32.6	292	15	AV063007	AV063007 AV063007	
19	151.6	32.2	287	15	AV065008	AV065008 AV065008	
20	148.4	31.5	276	15	AV078115	AV078115 AV078115	
21	148	31.4	285	15	AV032583	AV032583 AV032583	
22	144	30.6	306	15	AV069911	AV069911 AV069911	
23	142.4	30.2	300	16	AV169683	AV169683 AV169683	
24	139.4	29.6	300	17	AV239413	AV239413 AV239413	
25	138.4	29.4	294	15	AV067717	AV067717 AV067717	
26	138	29.3	299	15	AV067682	AV067682 AV067682	
27	135.6	28.8	293	15	AV076434	AV076434 AV076434	
28	130.4	27.7	279	15	AV087765	AV087765 AV087765	
29	124.8	26.5	281	15	AV062592	AV062592 AV062592	
30	124.8	26.5	567	21	AW338525	AW338525 xw80b03.x	
31	117.2	24.9	259	15	AV071444	AV071444 AV071444	
32	114	24.2	549	20	AW151778	AW151778 xf69b11.x	
33	92	19.5	515	13	AI1800476	AI1800476 tj14h05.x	
34	78	16.6	655	96	AQ377384	AQ377384 RPCI11-16	
35	63.8	13.5	325	20	AW142292	AW142292 EST292531	
36	57.2	12.1	188	15	AV077488	AV077488 AV077488	
37	56.6	12.0	468	8	AI129421	AI129421 qc38g11.x	
38	54.2	11.5	196	18	AV328761	AV328761 AV328761	
39	49.6	10.5	309	38	N83242	N83242 K4692F Huma	
40	47.6	10.1	438	9	AI247015	AI247015 qx52c10.x	
41	42.8	9.1	188	15	AV069285	AV069285 AV069285	
42	39.6	8.4	413	99	AQ592903	AQ592903 HS_5453_A	
43	37.6	8.0	442	1	AI129391	AI129391 zn85b03.s	
44	37.6	8.0	1101	121	CNS0039G	AL063921 Drosophil	
45	37.4	7.9	751	23	AW687654	AW687654 NF011G05R	

ALIGNMENTS

Db 245 TCTTTGGAGGAATGGATCCACCTGAAATATGTGATATAACAAAGTGTATCTCATATC 304
 Qy 301 TTTCAGAAACTGTTCCAGGACACACAAGATGGAGTTGAATCTCACTGTATGAAGA 360
 Db 305 TTTCAGAAACTGTTCCAGGACACACAAGATGGAGTTGAATCTCACTGTATGAAGA 364
 Qy 361 CACTTCTGCTGCCAAAGGAAGATGATGCTTCAAACCTCATCTGAAGAAAAGAT 420
 Db 365 CACTTCTGCTGCCAAAGGAAGATGATGCTTCAAACCTCATCTGAAGAAAAGAT 424
 Qy 421 GAAAATGGGATAAATCTGTAATGTTCACTCTCACTAACATCAAGT 471
 Db 425 GAAAATGGGATAAATCTGTAATGTTCACTCTCACTAACATCAAGT 475
 Result 2 AA892285/c
 Locus AA892285 646 bp mRNA EST 25-JAN-1999
 Definition EST196088 Normalized rat kidney, Bento Soares Rattus sp. cDNA clone
 Accession AA892285
 Version EST.
 Keywords EST.
 Source Rattus sp.
 Organism Rattus sp.
 Reference Lee,N.H., Glodek,A., Chandra,I., Mason,T.M., Quackenbush,J.,
 Authors Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
 Title Rat Genome Project: Generation of a Rat EST (REST) Catalog & Rat
 Gene Index
 Journal Unpublished (1998)
 Comment Contact: Lee, NH
 ATCC
 The Institute for Genomic Research
 9712, Medical Center Drive, Rockville, MD 20850, USA
 Tel: (301)-838-3529
 Fax: (301)-838-0208
 Email: nhlee@tigr.org
 Seq primer: M13-21.
 Features source
 1. .646
 /organism="Rattus sp."
 /db_xref="ATCC (inhost):2017880"
 /db_xref="taxon:10118"
 /clone="RKIAO60"
 /clone_lib="Normalized rat kidney, Bento Soares"
 /note="Organ: kidney; Vector: pT7T3pac; Site_1: EcoRI;
 Site_2: NotI"
 BASE COUNT 177 a 126 c 123 g 220 t
 ORIGIN
 Query Match 85.1%; Score 400.6; DB 7; Length 646;
 Best Local Similarity 91.8%; Pred. No. 4.4e-98;
 Matches 434; Conservative 1; Mismatches 35; Indels 3; Gaps 1;
 Features source
 1. .512
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone_lib="NIH_BMAP_M_S3.1"
 /dev_stage="27-32 days"
 /lab_host="DH10B (Life Technologies)"
 /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
 NIH_BMAP_M_S3.1 library; Not I; Site_1: Eco RI; The
 polylinker; Site_2: Not I; Site_1: Eco RI; The
 NIH_BMAP_M_S3.1 library is a subtracted library of a
 series, ultimately derived from a mixture of individually
 tagged normalized libraries from ten regions of the mouse
 179 CTGTGACCCCTCTGTGAAGGATAGTAAAYGTCACCCCTCTGTAAAGAACAGATCA 238

Db 399 CTGTGACCCCTATCTGTGAAGGATGGAGATGCTTACCCCTCTGTAAACAAATCA 340
 Qy 239 TTTCCTTGAGGAATGGATCCACCTGAAATATGTGATATAACAAAGTGTATCTCATAT 298
 Db 339 TTTCCTTGAGGAATGTGATCCACCTGAAATATGTGATATAACAAAGTGTATCTCATAT 280
 Qy 299 TCTTCAGAAACCGTGTCCAGGACACACAAGATGGAGTTGAATCTCACTGTATGAAG 358
 Db 279 TCTTCAGAAACCGTGTCCAGGACACACAAGATGGAGTTGAATCTCACTGTATGAAG 220
 Qy 359 GACACTTCTGCTGCCAAAGGAAGATGATGCTTCAAACCTCATCTGAAGAAAAGG 418
 Db 219 GACACTTCTAGCTGCCAAAGGAAGATGATGCTTCAAACCTGTTGAAAGGAAGG 160
 Qy 419 ATGAAATGGGATAAATCTGTAATGTTCACTCTCACTAACATCAAGT 471
 Db 159 ATGAAATGGGATAAATCTGTAATGTTCACTCTCACTAACATCAAGT 107
 Result 3 AW125102/c
 Locus AW125102 512 bp mRNA EST 22-OCT-1999
 Definition UI-M-BH2.1-apx-g-10-0-UI.s1 NIH_BMAP_M_S3.1 Mus musculus cDNA clone
 Accession AW125102
 Version AW125102.1 GI:6100632
 Keywords EST.
 Source house mouse.
 Organism Mus musculus
 Reference 1 (bases 1 to 512)
 Authors Bonaldo,M.F., Lennon,G. and Soares,M.B.
 Title Normalization and subtraction: two approaches to facilitate gene
 discovery
 Journal Genome Res. 6 (9), 791-806 (1996)
 Comment Contact: Chin, H
 MEDLINE
 9704477
 National Institute of Mental Health
 6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD
 Tel: 301 443 1706
 Fax: 301 443 9890
 Email: NEST@mail.nih.gov
 The sequence contained an oligo-dt track that was present in the
 oligonucleotide that was used to prime the synthesis of first
 strand cDNA and therefore this may represent a bona fide poly A
 tail. The sequence tag present in the cDNA between the NotI site
 and the oligo-dt track served to identify it as a clone from the
 normalized basal ganglia library cDNA Library Preparation: M.B.
 Soares Lab Clone distribution: NIH_BMAP cDNA clones will be made
 available by the means that is soon to be determined. When NIH
 determines the means for distribution of the BMAP cDNA clones, this
 record will be updated accordingly when that means is determined.
 The following repetitive elements were found in this cDNA sequence:
 17-81, >MSTD#LTR/MaLR
 Seq primer: M13 Forward
 PolyA=Yes.
 Features source
 1. .512
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone_lib="NIH_BMAP_M_S3.1"
 /dev_stage="27-32 days"
 /lab_host="DH10B (Life Technologies)"
 /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
 NIH_BMAP_M_S3.1 library; Not I; Site_1: Eco RI; The
 polylinker; Site_2: Not I; Site_1: Eco RI; The
 NIH_BMAP_M_S3.1 library is a subtracted library of a
 series, ultimately derived from a mixture of individually
 tagged normalized libraries from ten regions of the mouse
 179 CTGTGACCCCTCTGTGAAGGATAGTAAAYGTCACCCCTCTGTAAAGAACAGATCA 238

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brain (cerebellum, brain stem, olfactory bulbs, hypothalamus, cortex, amygdala, basal ganglia, pineal gland, striatum, hippocampus) after a series of subtractions to reduce the representation of cDNAs from which ESTs had already been generated. The following serially subtracted libraries were generated in this process: NIH_BMAP_M_S3.1, NIH_BMAP_M_S2, NIH_BMAP_M_S1. The subtracted library (NIH_BMAP_M_S3.1) was constructed as follows: PCR-amplified cDNA inserts from NIH_BMAP_M_S2 clones from which 3' ESTs had been derived was used as a driver in a hybridization with the NIH_BMAP_M_S2 library in the form of single-stranded circles. The remaining single-stranded circles (subtracted library) was purified by hydroxyapatite column chromatography, converted to double-stranded circles and electroporated into DH10B bacteria (LifeTechnologies) to generate the NIH_BMAP_M_S3.1 library. This procedure has been previously described (Bonaldo, Lennon and Soares, Genome Research 6:791-806, 1996)

TITLE	The WashU-HHMI Mouse EST Project
JOURNAL	Unpublished (1996)
COMMENT	Contact: Marra M/Mouse EST Project WashU-HHMI Mouse EST Project Washington University School of MedicineP 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: mouseest@watson.wustl.edu This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. MGI:924454 Seq primer: custom primer used High quality sequence stop: 410.

	BASE COUNT	Query Match	Score	DB	Length	ORIGIN
	135 a	1AQ_SEQ-IGIF	104 c	94 g	179 t	
Best Local Similarity	77.6%	77.6%	Score 365.6;	DB 20;	Length 512;	
Matches	365;	Conservative	99.7%;	Pred. No. 1.2e-88;		
				Mismatches 1;	Indels 0;	Gaps
Qy	106	GATCAAAGTGCCAGTGAACCCCAGACCTGATAATACTGTACAAGACAGTGAA	165			
Db	512	GATCAAAGTGCCAGTGAACCCCAGACCTGATAATACTGTACAAGACAGTGAA	453			
Qy	166	GTAAGAGGA CTGGCTGTGACCCCTCTGTGAA GGGATA TAGTAAAYGTCTACCCCTCTCCTGT	225			
Db	452	GTAAGAGGA CTGGCTGTGACCCCTCTGTGAA GGGATA TAGTAAATGTCTACCCCTCTCCTGT	393			
Qy	226	AAGAACAAAGATCATTTCCCTTGAGGAATGGGATCCACCTGAA AATATTGATGATA TACAA	285			
Db	392	AAGAACAAAGATCATTTCCCTTGAGGAATGGGATCCACCTGAA AATATTGATGATA TACAA	333			
Qy	286	AGTGATCTCATATCTTCAGAAACGGTCCAGGACACAACAAGATGGGTTGA ATCT	345			
Db	332	AGTGATCTCATATCTTCAGAAACGGTCCAGGACACAACAAGATGGGTTGA ATCT	273			
Qy	346	TCACTGTATGAAAGGACACTTCTGCTGCCAAAGGA AGATGATGATGCTTCAA ACTCATT	405			
Db	272	TCACTGTATGAAAGGACACTTCTGCTTGCCAAAGGA AGATGATGCTTCAA ACTCATT	213			
Qy	406	CTGAAAAAAAGGATGAAATGGGATA ATCTGTAATGTTCACTCTCACTA CTACAT	465			
Db	212	CTGAAAAAAAGGATGAAATGGGATA ATCTGTAATGTTCACTCTCACTA CTACAT	153			
Qy	466	CAA GT	471			
Db	152	CAA GT	147			
RESULT	4					
AI121020/c						
LOCUS	AI121020	474 bp	mRNA	EST	02-SEP-1998	
DEFINITION	ud69c02.x1	Sugano mouse liver mRNA	Mus musculus	cdna clone		
	IMAGE:1451138	3' similar to gb:D49949	Mouse mRNA	for IGIF precursor		
ACCESSION	AI121020	polypeptide (MOUSE);, mRNA sequence.				
VERSION	AI121020.1	EST.	GI:3521344			
KEYWORDS						
SOURCE	house mouse.					
ORGANISM	Mus musculus					
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;						
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus						
REFERENCE	1	(bases 1 to 474)				

RESULT 5 AA237736 AA237736 434 bp mRNA EST 03-MAR-1997
 LOCUS DEFINITION mx29901.rl Soares mouse NML Mus musculus cDNA clone IMAGE:681648 5'
 (MOUSE); mRNA sequence.

ACCESSION AA237736.1 GI:1861775
 VERSION AA237736.1 GI:1861775
 KEYWORDS EST.
 SOURCE house mouse.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 434)
 REFERENCE AUTHORS Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
 Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
 Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
 Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
 Waterston,R.
 COMMENT Unpublished (1996)
 TITLE JOURNAL Contact: Marra M/Mouse EST Project
 WashU-HMMI Mouse EST Project
 Washington University School of MedicineP
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: mouseest@watson.wustl.edu
 This clone is available royalty-free through LNL ; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 MGI:421352

putative full length read
 vector to vector length is 437
 Seq primer: -28ml3 rev2 ET from Amersham.

FEATURES source
 1. .434
 /organism="Mus musculus"
 /db_xref="taxon:10090"
 /clone="IMAGE:681648"
 /clone_1ib="Soares mouse NML"
 /tissue_type="Liver"
 /lab_host="DH10B"
 /note="Vector: pRT3D-Pac (Pharmacia) with a modified
 polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
 was primed with a Not I - oligo(dt) primer [5',
 TGTACCAATCTGAAGTGGGAGGGCCGAACTTTTTTTTTTTT 3'];
 double-stranded cDNA was ligated to Eco RI adaptors
 (Pharmacia), digested with Not I and cloned into the Not I
 and Eco RI sites of the modified pRT3 vector. Library
 constructed and normalized by Bento Soares and M.Fatima
 Bonaldo."
 BASE COUNT ORIGIN
 139 a 79 c 92 g 124 t

Query Match 65.5%; Score 308.6; DB 2; Length 434;
 Best Local Similarity 99.7%; Pred. No. 3e-73;
 Matches 308; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 163 GAGTAAGAGGACTGGCTGTGACCCTCTCTGTGAGGATAGTAAAYGCTTACCCCTCTC 222
 Db 1 GAGTAAGAGGACTGGCTGTGACCCTCTCTGTGAGGATAGTAAATGATGATA 60
 QY 223 TGTAGAACAGATCATTCCTTGAGGAATGGATCCACCTGAAGAATTGATGATA 282
 Db 61 TGTAGAACAGATCATTCCTTGAGGAATGGATCCACCTGAAGAATTGATGATA 120
 QY 283 GAAAGTGTCTATTCAGAACAGGTTCAGGACACAGAGGAGTTGAA 342
 Db 121 CAAAGTGTCTATTCAGAACAGGTTCAGGACACACAAGATGGAGTTGAA 180

RESULT 6 AI463005/c AI463005 469 bp mRNA EST 09-MAR-1997
 LOCUS DEFINITION vb89g05.x1 Soares mouse 3NbMS Mus musculus cDNA clone IMAGE:764216
 3', similar to gb:D49949 Mouse mRNA for IGIF precursor polypeptide
 (MOUSE); mRNA sequence.

ACCESSION AA463005 AA463005.1 GI:4317035
 VERSION AA463005.1 GI:4317035
 KEYWORDS EST.
 SOURCE house mouse.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 469)
 REFERENCE AUTHORS Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T.,
 Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person
 ,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter
 ,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R.,
 Waterston,R. and Wilson,R.
 COMMENT Unpublished (1999)
 TITLE JOURNAL Contact: Marra M/WashU-NCI Mouse EST Project 1999
 WashU-NCI Mouse EST Project 1999
 Washington University School of MedicineP
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: mouseest@watson.wustl.edu
 This clone is available royalty-free through LNL ; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 MGI:465136

FEATURES source
 1. .469
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="IMAGE:764216"
 /clone_1ib="Soares mouse 3NbMS"
 /sex="male"
 /tissue_type="Spleen"
 /dev_stage="4 weeks"
 /lab_host="DH10B"
 /note="Vector: pRT3D-Pac (Pharmacia) with a modified
 polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
 was primed with a Not I - oligo(dt) primer [5',
 TGTACCAATCTGAAGTGGGAGGGCCGCTGTTTTTTTTTTTTTTTTT 3'];
 double-stranded cDNA was ligated to Eco RI adaptors
 (Pharmacia), digested with Not I and cloned into the Not I
 and Eco RI sites of the modified pRT3 vector. RNA
 provided by Dr. Bertrand Jordan. Library went through
 three rounds of normalization, and was constructed by
 Bento Soares and M.Fatima Bonaldo."
 BASE COUNT ORIGIN
 132 a 99 c 90 g 144 t 4 others

Query Match 58.2%; Score 274; DB 10; Length 469;
 Best Local Similarity 90.7%; Pred. No. 6.9e-64;

Matches	311;	Conservative	1;	Mismatches	29;	Indels	2;	Gaps	2;
QY	131	CCAGACTGATAATACATGTACAAGACAGTGAAGTAAGGACTGGCTGTGACCCCTCT	190						
Db	469	CCAGCCTGATTATATCCATGGTCAAAGGCCAGTGAGTAAGAGGACTGCCTGTGCCCTTC	410						
QY	191	CTGTGAAGGATAGTAAAYGTCTACCTCTCTGTAAGAACAGATCATGCCCTTGAGG	250						
Db	409	TGTTGAAGGATAGTANAAATGTCTACCCCTNCTCCGTAAGAACAGGATCATTCCTTGAGG	350						
QY	251	AAATGGATCCA-CCTGAATAATTGATGATATACAAAGTGAICTCATATCTTCAGAAA	309						
Db	349	AAATGGATCCACCCCTGNAATAATGTGATACAAAGTGAICTCATATCTTCAGAAA	290						
QY	310	CGTTGTTCCAGGACACAACAGATG-GAGTTGAATCTTCACTGTATGAGGACACTTCT	368						
Db	289	CGTTGTTCCAGGACACAACAGATGNGAGTTGAATCTTCACTGTATGAGGACACTTCT	230						
QY	369	TGCTTGCCAAAAGGAAGATGATGCTTCAAACCTCTGAAAAAAAGGATGAAATGG	428						
Db	229	TGCTTGCCAAAAGGAAGATGATGCTTCAAACCTCTGAAAAAAAGGATGAAATGG	170						
QY	429	GGATAAATCTGTAATGTCACTCTCACTAACTTACATCAAGT	471						
Db	169	GGATAAATCTGTAATGTCACTCTCACTAACTTACATCAAGT	127						
RESULT 7									
LOCUS	AW558748	423 bp	mRNA	EST	02-AUG-2000				
DEFINITION	L0299E02-3	Mouse Newborn Ovary cDNA Library	Mus musculus	cdNA clone					
ACCESSION	AW558748	L0299E02	3'	mRNA sequence.					
VERSION	AW558748.1	GI:7204177							
KEYWORDS	EST.								
SOURCE	house mouse.								
ORGANISM	Mus musculus								
TITLE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.								
REFERENCE	1 (bases 1 to 423)								
AUTHORS	Tanaka,T.S., Jaradat,S.A., Lim,M.K., Kargul,G.J., Wang,X., Grahovac ,M.J., Pantano,S., Sano,Y., Piao,Y., Nagaraja,R., Doi,H., Wood,W.H. III, Becker,K.G. and Ko,M.S.H.								
JOURNAL	Genome-wide expression profiling of mid-gestation placenta and embryo using a 15,000 mouse developmental cDNA microarray								
COMMENT	Proc. Natl. Acad. Sci. U.S.A. 97 (16), 9127-9132 (2000)								
Laboratory of Genetics	Contact: George J. Kargul								
National Institute on Aging/National Institutes of Health	333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA								
Email:	cdna@gsun.grc.nia.nih.gov								
Plate:	L0299 row: E column: 02								
Seq primer:	-21M13 Forward								
High quality sequence stop:	423								
POLYA=Yes.									
FEATURES									
source	Location/Qualifiers								
1.	.423								
/organism="Mus musculus"									
/strain="C57BL/6J"									
/db_xref="taxon:10090"									
/clone="L0299E02"									
/clone_lib="Mouse Newborn Ovary CDNA Library"									
/sex="female"									
/lab_host="DHL0B"									
/note="Vector: pSPORT1 (Gibco/BRL Life Technology); Site_1: SalI; Site_2: NotI; Total RNAs were extracted from 7 Newborn Ovary. The double-stranded cDNA was synthesized by Gibco's kit with an Oligo(dT) primer [NotI primer-adapter from GibcoBRL] [5'-pGACTTGTCTAGATCGCGAGCGGCCCTTTTTTTT-3'] from 2.56ug of total RNA. The double-stranded cDNAs were treated with T4 DNA polymerase and purified by									
FEATURES									
source	Location/Qualifiers								
1.	.443								
/organism="Bos taurus"									
/db_xref="taxon:9913"									
Query Match									
Best Local Similarity	55.4%	Score	260.8;	DB	23;	Length	423;		
Matches	279;	Conservative	1;	Mismatches	13;	Indels	1;	Gaps	1;
QY	179	CTGTGACCCCTCTGTGAAGGATAGTAAAYGTCTACCCCTCTCTGTAGAACAGATCAA	238						
Db	423	CTGTGACCCCTCTGTGAAGGATAGTAAATGTCTACCCCTCTCTGTAGAACCCAGATCA	364						
QY	239	TTTCCTTTGAGGAATGGATCCACCTCAAAATATTGATGATATACAAAGTGAETCATAT	298						
Db	363	TTTCCTCTGAGGAATGGATCCACCTCAAAATATTGATGATATACAAAGTGAETCTCATAT	304						
QY	299	TCTTCAGAACAGTGTCCAGGACACAACAGATGGTTGAATCTTCACTGTATGAAG	358						
Db	303	TCGATCAGAACACGGTGTCCAGGACACACAAGATGGATGCTATGAACTCTTCACTGTATGAAG	244						
QY	359	GACACTTCTTGCTGCCAAAAGGAAGATGATGCTTCAAACCTCTG-AAAAAAAG	417						
Db	243	GACACTTCTAGCTGCCAAAAGGAAGATGATGCTTCAAACCTCTGAAAGAAAG	184						
QY	418	GATGAAATGGGATAATCTGTAATGTCACTCTCACTAACTTCACTCAAGT	471						
Db	183	GATAAAATGGGATAATCTGTAATGTCACTCTCACTAACTTACATAAAAGT	130						
RESULT 8									
LOCUS	AV597984	443 bp	mRNA	EST	06-AUG-2000				
DEFINITION	AV597984	Bos taurus cartilage fetus	Bos taurus	cdNA clone					
ACCESSION	E1CA035C10	3'	mRNA sequence.						
VERSION	AV597984								
KEYWORDS	EST.								
SOURCE	COW.								
ORGANISM	Bos taurus								
TITLE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea.								
REFERENCE	1 (bases 1 to 443)								
AUTHORS	Sugimoto,Y., Hirotsune,S., Takasuga,A., Itoh,R., Jitohzono,A. and Suzuki,H.								
JOURNAL	Unpublished (2000)								
COMMENT	Contact: Yoshihiko Sugimoto								
Animal Genetics Division									
Shirakawa Institute of Animal Genetics									
Odakura, Nishijo, Nishi-shirakawa, Fukushima 961-8061, Japan									
Tel: 81-248-25-5641									
Fax: 81-248-25-5725									
Email: kazusugi@coco.ocn.ne.jp									
Single pass sequencing.									
This clone was obtained from a polyA-deleted cDNA library.									
Location/Qualifiers									
1.	.443								
/organism="Bos taurus"									
/db_xref="taxon:9913"									

ethanol-precipitation. The cDNAs were ligated to Lone-linker LL-Sal3 (include SalI sequence). The cDNAs were purified by phenol/chloroform and separated from free linkers by Centrificon 100. Then, cDNAs were amplified by long-range high fidelity PCR using Takara's Ex Tag Polymerase. Then, the cDNAs were purified by phenol/chloroform and by Centrificon 100. The cDNAs were digested with SalI and NotI enzymes. Then, the cDNAs were size selected by Gibco's Size Fractionation Column. The cDNAs were cloned into SalI/NotI site of pSPORT1 plasmid vector. The DH10B E. coli host was transformed with the ligation mixture by chemical method. The library was constructed by Xiaohong Wang and Yulan Piao."

BASE COUNT
ORIGIN
116 a 84 c 81 g 142 t

```

/clone="E1CA035C10"
/clone_lib="Bos taurus cartilage fetus"
/tissue_type="cartilage"
/dev_stage="fetus"
/note="vector: pZL1; Site_1: Sal1; site_2: Not1; Poly A
was deleted from a Not1 site"
134 a 77 c 79 g 153 t

```

50.9%; Score 239.8; DB 19; Length 443;
 75.5%; Pred. No. 1.2e-54;
 conservative 1; Mismatches 98; Indels 6; Gaps 2;

FEATURES	source	Location/Qualifiers
	1. .357	1.
	/organism="Mus musculus"	.357
	/db_xref="C57BL/6J"	
	/clone="UI-M-BH1-amr-f-09-0-UT"	
	/clone_lib="NIH_BMAP_M_S2"	
	/dev_stage="27-32 days"	
	/lab_host="DH10B (Life Technologies)"	
	/note="vector: pt7T3D-Pac (Pharmacia) with a modified	
	polylinker; Site_1: Not I; Site_2: Eco RI; The	
	NIH_BMAP_M_S2 library is a subtracted library	
	derived from a mixture of normalized libraries from ten	
	regions of the mouse brain (cerebellum, brain stems,	
	olfactory bulbs, hypothalamus, cortex, amygdala, basal	
	ganglia, pineal gland, striatum, hippocampus). The driver	
	used for subtraction consisted of a pool of 5,000 clones	
	from the NIH_BMAP_M_S1 library and a pool of 2,000 clones	
	obtained from non-normalized and normalized mouse brain	
	spinal cord libraries.	
	TAG_LIB=NIH_BMAP_M_S2	
	TAG_TISSUE=brain-stems	
	TAG_SEQ=TCATG"	

Seq primer: M13 Forward
 POLYA=Yes.

50.9%; Score 239.8; DB 19; Length 443;
 75.5%; Pred. No. 1.2e-54;
 conservative 1; Mismatches 98; Indels 6; Gaps 2;

TATAAATGACCAAGTCTCTCGTTGACAA---AAGACAGCCCTGGTTCGAGGAT 93

TTGAATGACCAAGTCTCTCGTTGACAA---AAGACAGCCCTGGTTCGAGGAT 93

TGATATGTGATCAAAGTGCCAGTGAACCCAGACAGACTGATAATACATGTAC 153

TGATATGTGATCAAAGTGCCAGTGAACCCAGACAGACTGATAATACATGTAC 153

TGATCTGACTGTGTCAGATAATGCACCCAGACATATTATCATATATATGTAT 384

TGATCTGACTGTGTCAGATAATGCACCCAGACATATTATCATATATATGTAT 384

TAGTGAAGTAAGAGGACTGGCTGTGACCCCTCTGTGAAGGATAGTAAAYGCT 213

TAGTGAAGTAAGAGGACTGGCTGTGACCCCTCTGTGAAGGATAGTAAAYGCT 213

TAGGCTCACTAGAGGTCTGGCGTAACCATCTCTGTGCAAGTGTAAAGAAATGCT 264

TAGGCTCACTAGAGGTCTGGCGTAACCATCTCTGTGCAAGTGTAAAGAAATGCT 264

TCTCTGTGAGAACAGATCATTTCTTGTGAGGAATGGGATCCACCTGAAATT 273

TCTCTGTGAGAACAGATCATTTCTTGTGAGGAATGGGATCCACCTGAAATT 273

TCTCTGTGAGAACAGATCATTTCTTGTGAGGAATGGGATCCACCTGAAATT 204

TCTCTGTGAGAACAGATCATTTCTTGTGAGGAATGGGATCCACCTGAAATT 204

TCTCTGTGAGAACAGATCATTTCTTGTGAGGAATGGGATCCACCTGAAATT 330

TCTCTGTGAGAACAGATCATTTCTTGTGAGGAATGGGATCCACCTGAAATT 330

TGAGAAGAAGTGCATCATTTCTTCAAGAAGTGTCCAGGACATGATGATAAG 144

TGAGAAGAAGTGCATCATTTCTTCAAGAAGTGTCCAGGACATGATGATAAG 144

GTGAACTCTCACTGTATGGACACTTCTGCTTGCCAAAAGGAAGATGAT 390

GTGAACTCTCACTGTATGGACACTTCTGCTTGCCAAAAGGAAGATGAT 390

ATTTGAGTCTTCAAGGTACTTCTAGCTTGTAAAGAGAAATGAC 84

ATTTGAGTCTTCAAGGTACTTCTAGCTTGTAAAGAGAAATGAC 84

CAAACCTATTGAAAAAACAGGATATAAGAGATAATCTGTATGTTCACT 450

CAAACCTATTGAAAAAACAGGATATAAGAGATAATCTGTATGTTCACT 450

CAAACCTATTGAAAAAACAGGATATAAGAGATAATCTGTATGTTCACT 24

oligonucleotide that was used to prime the synthesis of this strand cDNA and therefore this may represent a bona fide Poly A tail. The sequence tag present in the cDNA between the Not1 site and the oligo-dT track served to identify it as a clone from the normalized brain stems library cDNA Library Preparation: M.B. Soares Lab Clone distribution: NIH BMAP cDNA clones will be made available by the means that is soon to be determined. When NIH determines the means for distribution of the BMAP cDNA clones, this record will be updated accordingly when that means is determined. The following repetitive elements were found in this cDNA sequence:
 18-84, >MSTD#LTR/MALR
 Seq primer: M13 Forward

Query Match 44.28; Score 208; DB 19; Length 357;
 Best Local Similarity 100.0%; Pred. No. 4.5e-46;
 Matches 208; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

BASE COUNT

ORIGIN

100 a 71 c 59 g 127 t

Query Match 44.28; Score 208; DB 19; Length 357;

Best Local Similarity 100.0%; Pred. No. 4.5e-46;

Matches 208; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 264 TGAATATGTGATATAACAAGTGTCTCATATTCTTCAGAACCGTGTCCAGGACA 323

Db 357 TGAATATGTGATATAACAAGTGTCTCATATTCTTCAGAACCGTGTCCAGGACA 298

QY 324 CAACAAGATGGAGTTGAATCTCACTGTATGAAGGACACTTCTGCTTGCCAAAGGA 383

Db 297 CAACAAGATGGAGTTGAATCTCACTGTATGAAGGACACTTCTGCTTGCCAAAGGA 238

QY 384 AGATGATGGCTTCAACTCATCTGAAAAAGGATGAAATGGGATAATCTGTAT 443

Db 237 AGATGATGGCTTCAACTCATCTGAAAAAGGATGAAATGGGATAATCTGTAT 178

QY 444 GTCACTCTCACTTACATCAAAGT 471

Db 177 GTCACTCTCACTTACATCAAAGT 150

RESULT 10

AT176343/c

LOCUS AT176343 369 bp mRNA

DEFINITION EST219926 Normalized rat ovary, Bento Soares Rattus sp. cDNA clone

ACCESSION ROVBQ38 3' end, mRNA sequence.

VERSION AT176343

KEYWORDS EST.

SOURCE Rattus sp.

ORGANISM Rattus sp.

Mus musculus

Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

aldo, M.F., Lennon, G. and Soares, M.B.

malization and subtraction: two approaches to facilitate gene

covery

ome Res. 6 (9), 791-806 (1996)

44477

tact: Chin, H

ional Institute of Mental Health

1 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD

92-9643, USA

: 301 443 1706

: 301 443 9890

il: mEST@mail.nih.gov

sequence contained an oligo-dT track that was present in the

	COMMENT
REFERENCE	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
AUTHORS	1 (bases 1 to 369)
TITLE	Rat Genome Project: Generation of a Rat EST (REST) Catalog & Rat Gene Index
JOURNAL	Unpublished (1998)
COMMENT	On Oct 8, 1998 this sequence version replaced gi:3726981.
ATCC	The Institute for Genomic Research 9712, Medical Center Drive, Rockville, MD 20850, USA
TEL:	Tel: (301)-838-3529
FAX:	Fax: (301)-838-0208
EMAIL:	Email: nhlee@tigr.org
SEQ PRIMER:	Seq primer: M13-21.
FEATURES	Location/Qualifiers
SOURCE	1. . 369 <organism="Rattus sp." <db_xref="taxon:10118" <clone="ROVBQ38" <note="Organ: ovary; Vector: pT/T3Pac; Site_1: ECORI; Site_2: NotI" BASE COUNT ORIGIN
114 a 64 c 61 g 130 t	
Query Match	44.0%; Score 207.4; DB 9; Length 369;
Best Local Similarity	91.3%; Pred. No. 6.6e-46;
Matches	220; Conservative 0; Mismatches 21; Indels 0; Gaps 0;
QY	231 CAAGATCATTCTTGAGGAATGGATCCACCTGAAATATGTGATATAAAGTGA 290
DB	369 CAAATCATTTCTTGAGGAATGAAATATGTGATATAAAAGTGA 310
QY	291 TCTCATATTCTTCAGAACGTTCCAGGACACACAAGATGGAGTTGAATCTTCACT 350
DB	309 TTTCAAATTCTTCAGAACGTTGCAGACCAACAAATGGAAATTGAAATCTCCCT 250
QY	351 GTATGAGGACACTTCTTGCCAAAGGAAGATGATGCTTCAACTCATCTGAA 410
DB	249 GTATGAGGACCTTTAGCTTGCCAAAGGAATGATGCTTCAACTCGTTAA 190
QY	411 AAAAAGGATGAAATGGGATAATCTGTAATGTTCACTCTACTAACTTACATCAAAG 470
DB	189 AAGGAAGGATGAAATGGGATAATCTGTAATGTTCACTTACATCACAG 130
QY	471 T 471
DB	129 T 129
RESULT	11
LOCUS	AI835755 342 bp mRNA EST 14-JUL-1999
DEFINITION	UT-M-A10-aan-g-11-0-UI.s1 NIH_BMAP_MBS Mus musculus CDNA clone
ACCESSION	UI-M-A10-aan-g-11-0-UI 3', mRNA sequence.
VERSION	AI835755
KEYWORDS	EST.
SOURCE	house mouse.
ORGANISM	Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
REFERENCE	1 (bases 1 to 342)
AUTHORS	Bonaldo, M.F., Lennon, G. and Soares, M.B.
TITLE	Normalization and subtraction: two approaches to facilitate gene discovery
JOURNAL	Genome Res. 6 (9), 791-806 (1996)
MEDLINE	9704477
RESULT	12
LOCUS	AV066410 335 bp mRNA EST 24-JUN-1999
DEFINITION	AV066410 Mus musculus small intestine C57BL/6J adult Mus musculus CDNA clone 2010109E01, mRNA sequence.
ACCESSION	AV066410

VERSION	AA245600.1	GI:	1876519
KEYWORDS	EST.		
SOURCE	house mouse.		
ORGANISM	Mus musculus		
REFERENCE	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus; house mouse.		
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Carninci,P., Shibata,K., Ozawa,Y., Konno,H., Itoh,M., Aizawa,K., Akahira,S., Akiyama,J., Fukuda,S., Fukunishi,Y., Funayama,T., Hara,A., Hayatsu,H., Hori,F., Ishikawa,T., Itoh,M., Izawa,M., Kawai,J., Kikuchi,N., Kojima,Y., Matsuyama,T., Niitsuma,H., Oda,H., Owa,C., Sato,K., Shibata,Y., Shigemoto,Y., Shiraki,T., Sugabe,Y., Sugahara,Y., Suzuki,H., Suzuki,H., Tateno,M., Tomaru,Y., Tominaga,N., Watanabe,S., Yagane,M., Yamamura,T., Yokota,T., Yoshino,M., Muramatsu,M., Okazaki,Y. and Hayashizaki,Y.		
TITLE	RIKEN Mouse ESTS		
JOURNAL	Unpublished (1999)		
COMMENT	Contact: Chie Owa Genome Science Laboratory 3-1-1 Koyodai, Tsukuba, Ibaraki 305-0074, Japan Tel: 81-298-36-9145 Fax: 81-298-36-9098 Email: genome.res@rci.riken.go.jp Please visit our web site (http://genome rtc.riken.go.jp/) for further details.		
FEATURES	Location/Qualifiers		
source	1. .335 'organism="Mus musculus" 'strain="C57BL/6J" 'db_xref="taxon:10090" 'clone="2010109E01" 'clone_1lib="Mus musculus small intestine C57BL/6J adult" 'sex="male" 'tissue_type="small intestine" 'dev_stage="adult" BASE COUNT ORIGIN a 109 a 59 c 67 g 100 t		
FEATURES	Trace considered overall poor quality		
source	Seq primer: -28ml3 rev2 ET from Amersham High quality sequence stop: 1. Location/Qualifiers		
source	1. .289 'organism="Mus musculus" 'lab_host="DH10B" 'db_xref="IMAGE:681672" 'clone_1lib="Soares mouse NML" 'tissue_type="Liver" 'note="vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand was primed with a Not I - oligo(dt) primer [5' TGTATCCAACTGAACTGGAGGGGCCGCAGTCCTTTTTTTTTTTT 3']; double-stranded CDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library constructed and normalized by Bento Soares and M.Fatima Bonaldo."		
BASE COUNT	77 a 51 c 75 g 86 t		
ORIGIN	Query Match 40.7%; Score 191.6; DB 15; Length 335; Best Local Similarity 95.6%; Pred. No. 1.2e-41; Matches 197; Conservative 0; Mismatches 9; Indels 0; Gaps 0;		
Qy	266 AAATATTGATGATGAAAGTGATCATTCCTCGAACACGTGTCAGGACACA 325 1 AAAATATTGATGATGAAAGTGATCATTCCTCGAACACGTGTCAGGACACA 60		
Qy	326 ACAAGATGGGTGGAATCTCACTGTTGAGGACACTTCTTGCTGCCAAAGGAAG 385 61 ACAAGATGGGTGGAATCTCACTGTTGAGGACACTTCTTGCTGCCAAAGGAAG 120		
Db	ATGATGCTTCAACTCACTTCTGAAAAAAGGATGAAATGGGATAAATCTGTAATGT 445 121 ATGAGCTTCACACTGATGAAAGGATGAAATGGGATAAATCTGTAATGT 180		
Qy	446 TCACTCTCACTAATCTACATCAAAGT 471 181 TCACTCTCACTAATCTACATCAAAGT 206		
RESULT	13		
AA245600	AA245600 289 bp mRNA EST 10-MAR-1997		
LOCUS	mx30a01.1 soares mouse NML Mus musculus cDNA clone IMAGE:681672 5'		
DEFINITION	similar to gb:D49949 Mouse mRNA for IGF precursor polypeptide (MOUSE); mRNA sequence.		
ACCESSION	AA245600		

RESULT 14
AI046315

LOCUS AI046315 505 bp mRNA EST 08-JUL-1998

DEFINITION ud69c02.y1 Sugano mouse liver mlia Mus musculus cDNA clone

IMAGE:1451138 5' similar to gb:D49949 Mouse mRNA for IGF precursor polypeptide (MOUSE); mRNA sequence.

ACCESSION AI046315

VERSION AI046315.1 GI:3294602

KEYWORDS EST.

SOURCE house mouse.

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 505)

AUTHORS Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., DeM., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and Waterston,R.

TITLE The WashU-HMM Mouse EST Project

JOURNAL Unpublished (1996)

COMMENT Contact: Marra M/Mouse EST Project

Washington University School of MedicineP

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: mouseest@watson.wustl.edu

This clone is available royalty-free through LIRL ; contact the IMAGE consortium (info@image.lnl.gov) for further information.

MGI:924454

Seq primer: custom primer used

High quality sequence stop: 385.

Location/Qualifiers

FEATURES source

1. .505

/organism="Mus musculus"

/strain="C57BL"

/db_xref="taxon:10090"

/clone="IMAGE:1451138"

/clone_lib="Sugano mouse liver mlia"

/sex="female"

/dev_stage="adult"

/lab_host="DH10B"

/note="Organ: liver; Vector: pME18S-FL3; Site_1: DraIII (CACTGTGTG); Site_2: DraIII (CACCATGTG); 1st strand cDNA was primed with an oligo(dT) primer [ATGGGCCCTTTTTTTTTTT]; double-stranded cDNA was ligated to a DraIII adaptor [TGTTGGCTACTGG], digested and cloned into distinct DraIII sites of the pME18S-FL3 vector (5' site CACTGTGTG, 3' site CACCATGTG). XbaI should be used to isolate the cDNA insert. Size selection was performed to exclude fragments <1.5kb. Library constructed by Dr. Sumio Sugano (University of Tokyo Institute of Medical Science). Custom primers for sequencing: 5' end primer CTTCTGCTAAAGCTGCG and 3' end primer CGACCTGCAGCTCGAGCACA."

BASE COUNT ORIGIN

143 a 129 c 116 g 117 t

Query Match 35.4%; Score 166.8; DB 8; Length 505;

Best Local Similarity 98.8%; Pred. No. 6.8e-35; Matches 168; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 AACTTGGCCGACTTCAGTGTACAACCGCAGTAATACGGAATATAATGCCAAGTTCTC 60

Db 336 AACTTTGGCCGACTTCAGTGTACAACCGCAGTAATACGGAATATAATGCCAAGTTCTC 395

QY 61 TTCTGGTACAAAAGACAGCCTGTTGAGGATATGACTGATATTGATCAAAGTGCAGT 120

Db 396 TTCTGGTACAAAAGACAGCCTGTTGAGGATATGACTGATATTGATCAAAGTGCAGT 455

QY 121 GAACCCCAGACAGCAGCTGTTGAGGATATGACTGATATTGATCAAAGTGCAGT 170

Db 456 GAACCCCAGACAGCAGCTGATTATACATGTACAAGTGAAGTAAG 505

RESULT 15

LOCUS AV597985

DEFINITION AV597985 BOS taurus cartilage fetus Bos taurus cDNA clone

EST. E1CA035C10 5', mRNA sequence.

ACCESSION AV597985

VERSION AV597985.1 GI:9715480

KEYWORDS EST.

AUTHORS Bos taurus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos. 1 (bases 1 to 574)

REFERENCE Sugimoto,Y., Hirotsune,S., Takasuga,A., Itoh,R., Jitohzono,A. and Suzuki,H.

COMMENT bovine CDNA sequencing

Contact: Yoshikazu Sugimoto

Animal Genetics Division

Shirakawa Institute of Animal Genetics

Odakura, Nishigo, Nishi-shirakawa, Fukushima 961-8061, Japan

Tel: 81-248-25-5641

Fax: 81-248-25-5725

Email: kazusugi@cocca.ocn.ne.jp

This clone was obtained from a polyA-deleted cDNA library.

Single pass sequencing.

Location/Qualifiers

FEATURES source

1. .574

/organism="Bos taurus"

/db_xref="taxon:9913"

/clone="E1CA035C10"

/clone_lib="Bos taurus cartilage fetus"

/tissue_type="cartilage"

/dev_stage="fetus"

/note="Vector: pZL1; Site_1: Sall; Site_2: Not1; Poly A was deleted from a Not1 site"

BASE COUNT ORIGIN

173 a 126 c 114 g 161 t

Query Match 33.0%; Score 155.6; DB 19; Length 574;

Best Local Similarity 72.9%; Pred. No. 7.5e-32; Matches 213; Conservative 1; Mismatches 75; Indels 3; Gaps 1;

QY 2 ACTTTGGCCGACTTCAGTGTACAACCGCAGTAATACGGAATATAATGCCAAGTTCTC 61

Db 280 ACTTTGGCAAACCTGAACCTAAGCTCTCAATCATACGAAATTGACCAAGTTCTC 339

QY 62 TCGTTGACAAAAGA---CAGCTGTGTCAGGATATGACTGATATTGATCAAAGTGCCA 118

Db 340 TCATTAACCGGAAATCAACCTGTCTTGAGGATATGCCATGTCAGTCTGACTGTTGAGATA 399

QY 119 GTGAACCCCCAGACAGCAGACTGATAATATACATGTACAAGACAGTGAAGTAAGGAGCTGG 178

Db 400 ATGCACCCAGACCCATATTATCATATATATGTATAAGGACAGCCTCACTAGAGGTCTGG 459

QY 179 CTGTGACCCCTCTGTGAAGGATAGTAAAYGTCACCCCTCTCCCTGTAAGAACAGATCA 238

Db 460 CCCTAACCATCTCTGTGTCAGTGTAAAGAACATGTCTACTCTCTCTGAGAACAAATTG 519

QY 239 TTCCCTTGAGGAATGGATCCACCTGAAATATTGATGATATACAAAGTGA 290

Db 520 TTCCCTTAAGGAATATGAAATCCCTCCTGATAACATTGATAATGAAAGAAGTGA 571

Sat Nov 25 20:12:56 2000

us-09-373-230-1.rst

